

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 15:00:11 ; Search time 2786 Seconds
(without alignments)
15919.364 Million cell updates/sec

Title: US-09-815-923-3
Perfect score: 1764
Sequence: 1 atgcgcgcgtcgacgcgc.....ctaccctatgcacactgtga 1764

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

al number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1764	100.0	1764	US-09-815-923-3	Sequence 3, Appl1
2	891.2	50.5	2470	US-60-173-464-7056	Sequence 7056, Ap
3	891.2	50.5	2471	US-09-614-150-8705	Sequence 8705, Ap
4	891.2	50.5	2471	US-60-191-637-8731	Sequence 8731, Ap
5	891.2	50.5	2471	US-60-191-681-6790	Sequence 6790, Ap
6	891.2	50.5	2473	US-60-167-217-8786	Sequence 8786, Ap
7	579.8	32.9	2745	US-60-360-207-11577	Sequence 11577, A
8	579.4	32.8	2278	US-07-778-231-6	Sequence 6, Appl1
9	554	31.4	1890	PCT-US00-20638-11	Sequence 1068, Ap
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11	552.6	31.3	2099	US-09-440-302B-1068	Sequence 1068, Ap
12	552.6	31.3	2099	US-09-622-503-2	Sequence 2, Appl1
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14	552.4	31.3	1893	US-60-226-176-2040	Sequence 2040, Ap
15	552.4	31.3	1893	US-60-226-176-2045	Sequence 2045, Ap
16	552.4	31.3	1893	US-60-233-468-2040	Sequence 2040, Ap
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18	552.4	31.3	1893	US-60-313-371-2040	Sequence 2040, Ap
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36 552.4 31.3 4305 41 US-10-198-846-11010 Sequence 2571, Ap
37 525.4 29.8 1831 65 US-60-213-177-1027 Sequence 11010, A
38 522.4 29.6 1854 1 PCT-US00-35491-1 Sequence 1027, Ap
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41 522.4 29.6 1854 29 US-09-750-609-1 Sequence 11, App1
42 522.4 29.6 1854 61 US-60-173-682-1 Sequence 1, App1
43 522.4 29.6 1854 61 US-60-173-682-1 Sequence 11, App1
44 522.4 29.6 1983 3 US-07-676-980B-1 Sequence 1, App1
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ALIGNMENTS

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RESULT 1
US-09-815-923-3
: Sequence 3, Application US/09815923
: GENERAL INFORMATION:
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: APPLICANT: GILL, Sarjeet S.
: APPLICANT: Ross, Linda S.
: TITLE OF INVENTION: The Regents of the University of California
: TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as Novel
: FILE REFERENCE: 023070-093800US
: CURRENT APPLICATION NUMBER: US/09/815,923
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO: 3
: LENGTH: 1764
: TYPE: DNA
: ORGANISM: Manduca sexta
: FEATURE:
: OTHER INFORMATION: serotonin transporter
US-09-815-923-3
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Query Match 100.0%; Score 1764; DB 31; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 121 TGGGCGAAGAGCAGAGATCTCTGCGGTGGTGGATTCGAGTGGATCTTGGTAAC 180
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DB 181 GTGTGGCGATTCCTCTACATCTGTTACCAAGATGAGGCGGTGCGTCTGATCCGTAC 240
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QY	1441	GAAGATGTGAGGACCATGCTGGGGACACCCCTGGATGATTCTGGAGGACCTGTTGGTCT	1500
Db	1441	GAAGATGTGAGGACCATGCTGGGGACACCCCTGGATGATTCTGGAGGACCTGTTGGTCT	1500
QY	1501	TACATCAAGTCCCGTATTCTTGCTGGTGTCTGTTGCTGTTCTCCGTTCTGGCACAGGAGAG	1560
Db	1501	TACATCAAGTCCCGTATTCTTGCTGGTGTCTGTTGCTGTTCTCCGTTCTGGCACAGGAGAG	1560
QY	1561	ATGCTCGCGGGGGAATACACCTATCCCTCATGAGTCATACACCGTAAGGCTGGGTATGACC	1620
Db	1561	ATGCTCGCGGGGGAATACACCTATCCCTCATGAGTCATACACCGTAAGGCTGGGTATGACC	1620
QY	1621	GGCACCAACCGTCTGTCGATCTCTCTTTACATTTATCTACAACAGCTCATGACTCTCGGC	1680
Db	1621	GGCACCAACCGTCTGTCGATCTCTCTTTACATTTATCTACAACAGCTCATGACTCTCGGC	1680
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QY	1741	GACTCTACCCATGACCAACCTGTGA	1764
Db	1741	GACTCTACCCATGACCAACCTGTGA	1764

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RESULT 2
US-60-173-464-7056
: Sequence 7056, Application US/60173464
: GENERAL INFORMATION:
: APPLICANT: Li, Peter W. D.
: TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
: FILE OF INVENTION: THEREOF
: FILE REFERENCE: CL000173
: CURRENT APPLICATION NUMBER: US/60/173,464
: CURRENT FILING DATE: 1999-12-29
: NUMBER OF SEQ ID NOS: 30269
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7056
: LENGTH: 2470
: TYPE: DNA
: ORGANISM: Drosophila
US-60-173-464-7056

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Very Match	50.5%	Score 891.2	DB 61	Length 2470
Best Local Similarity	71.7%	Pred. No. 2.1e-212		
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				Gaps 1

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QY	82	GTGGTGTGTGCGCTTACCCCGGCGCGGACCGCGAGACTGGGGCAAGAGCAGAGTTC	141
Db	190	AFTTCGTGGTGCTCCGTCGACGAGAGGAGCTCCGAGACTCGGGGACAGAGCGGAGTTC	249
QY	142	CTGCGGGGGGTGGTGGATCGCATGTGATCTTGATTAACGTGGGATTCCTCCATATC	201
Db	250	CTCCTGGCGGTGATTTGGGTTCCGATTCGATCTGGGCATGTGTGGGCTTCCGTCATATC	309
QY	202	TGTTACCGAATGAGGGCGGTGCGCTTCCTGATCCGCTACCTGGCTATATGCTGCTGTTTGGC	261
Db	310	TGCTATCAGAAAGGAGCGGCGGCCCTTCCTGGGTGCCCTACTGCTCTTCTCATCTTCGGT	369
QY	262	GGGCGCGCGCGTGTCTTCTCGAATCTGGGCGCGGGCCAGTACACCGCTCGGCGTCCGC	321
Db	370	GGACTGCCCTGTTTCTATCATGGAGCTGGGCGCGGCGCACTTCACCGCAGTGTGGTTCCTC	429

OY	322	ACTCTCTGGAAGCGGATGTGCCCCCGCTTAAAGGAGTGGGCTATGCCATCTGCAATGATC	381
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OY	382	GACATCTCATATGAGCGCATGTACTACAAACAGATCATCGATGGAGGGGTGTATTAACTCGATC	441
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OY	442	GCTTCTCGGGCTCTATAAAGCTCTGTGCTGCCATGAGCCAGCGTCGCACAAAGATGGGAAC	501
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OY	502	ACGCCGCTGTGCACGCGCGGTACCTCAACCTCAAGACTTAATCTAACTCTTCTACACCGGAG	561
Db	601	ACTGGAACCTGCAATCAGGTGACCAAGTAGAACCTTACAGGAACCTGGCCACAGTGGCCGGCC	660
OY	562	AAGCAGTTCTTGCAGACGTATATGTATTTGAGCAGCACACAACTTAACGCGCTCGATGCATAG	621
Db	661	AAGGAGTCTTTTGACGGAAGGTTTGTGAGACTCAACAAGGCAACGCGGCTGGACTTCATG	720
OY	622	GAGCCGATCAACCGCTCGCTGTGTGTGTTGCGGGGCTTTGTCTCTCGTCTAATTC	681
Db	721	GGTCGGGTAAGGCCACCGCTGGCACCTGCTCTTCGCGGGCTTTGTCTCGGTCTACTTC	780
OY	682	TCTTGTGGAAGAGGTCAAGAGTGTCTGGCAAGGTGTGTGGGTGACACTCTGGCCCCG	741
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OY	742	TACGTTGTCCTCATTTCTGCTGGCGAAGAGCGTCAAGCTTCCAGAGACGACGAGGAGGC	801

QY	802	ATPAGGCTACTACCTTACCACAGAGTGGGACAAATGTGCAAAACCTTAAGGTATGATATGC	861
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QY	922	AGCTACACAAAGTTTCAACAAACACTGCTACAGGGGCGGCTCATCTTTCTTCTTCAAC	981
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QY	1042	GTTACAGAACAGAGCATATGAGAGGTTGGCCCTGAAAGCCCTGAGCTGGTTCATTCGTG	1100
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Db	1261	ATGCTGATATACCCTGGGACTTGACAGCACTTTTGGCGATTTGGAGGCACTGATTAACACCG	1320
QY	1222	CTTTGCGAGCAATATCTCTCGAGTGTTAAGCAGACATCTCGAAGTATTTGTGGCTTACTG	1281
Db	1321	CTTTGCGAGCAATATCCGAGTGTATGCGAGGCGGAGGCGGAGAGAGCTTTGTCTCTGGCTC	1380
QY	1282	CTTCTGTTTCATCTATATTTGGGCTTGCCCAACACCAATACAGTGGTGTATACCTGTA	1344
Db	1381	CTGGCTTTCATCTTCTGTTGGGCTTCCCAAGATGACCTGAGGGGCTGTGGTGTCTC	1440
QY	1342	GACCTACTCAATGTGTATGGCCCTTGGATTTGGAGTATTAATTCGTGTATTTGCTAGAGCT	1400
Db	1441	AACTTCCTGAAAGTCTACGGAACCGGGTTGGCAATCCTTTGTGTCTTGGTGGAGCA	1500
QY	1402	GCGGCGCTGTGCTGGGTATGGCTGCACCCGGTTCTTGAAAGATGTAGACCACTGCTG	1461

Db	1381	CTGGCTTTCATCTTCCTGTCGGCCCTTCCACAGATGACATACGGTGGCGTGTGCTGTGTC	1440
Oy	1342	GACCTACTCAATGTGTATGCGCCCTGGATGTGGCGATTCATATTCGTGTATTTGCTAGAGCT	1401
Db	1441	AACTTTCCGTAATGTCTACAGGACCCGGGTGGCCATCCCTTTGTGTCTTCGTGTGAGCA	1500
Oy	1402	GCGGGCGTGTCTGGGTGTATGCGCTGCACCGGTTCTCTGAAGATGTGAGACCATCTG	1461
Db	1501	GCCGGAGCTTTTGTGTCTACGGAGTGGACCGCTTCAAGCTGGATGTGTGAACAGATGCTG	1560
Oy	1462	GGGACACACCCCTGGATGGTGTGGAGGACCTGTTGGTTCATCAACAGCCCGTATTCCTG	1521
Db	1561	GGCAGACAGCCAGCGTTATTTCTGGCGGATTCCTGCTGACGTACATACAGCCCTGTGTTCTG	1620
Oy	1522	CTGGTGTCTGTTCTGTTCTCCGTTCTGGCACACGAGAGATGCTGGCGGGAATACACC	1581
Db	1621	CTGACCAATTCATTTTCTCCATCATCATGAGGCTACAAAGAGAGTCTCGGGAGAGATCTAC	1680
Oy	1582	TATCCCTCAGGTCTATCACCGGTAGCGTGGGTGATGACGGCACCACCCGTCGTGCAATT	1641
Db	1681	TACCCGGAGCTGAGACTACAGGTGGGCGTGGCGGTACACTCTGTCGTCTCTGCATC	1740
Oy	1642	CCCTTTACATATCTACAAACCTGCTATCAC	1673
Db	1741	CCCATGTACATTATCTACAAAGTCTTCTTCCG	1772

```

RESULT 4
US-60-191-637-8731
; Sequence 8731, Application US/60191637
;
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8731
;
; LENGTH: 2471
;
; TYPE: DNA
;
; ORGANISM: DROSOPHILA
US-60-191-637-8731

```

Query Match	50.5%:	Score 81.2:	DB 63:	Length 2471:
Best Local Similarity	71.7%:	Pred. No.1e-212:		
Matches 1185:	Conservative 0:	Mismatches 458:	Indels 9:	Gaps 1:
22	CCCGGGCCACCGGGCCACCTCGATGATTTCTCTGATCTACACCGGCTGCAAAAGCCGCTTG	81		
130	CACACGACGCCCCGCCAAGCTACCGATCACTGCCCCCAAGCTGGCCAAACAGCAGCGC	189		
82	GTGGTGTGTGTGCTTACGCGCGCGCGGCGAGCCAGACCTGGGCGAAGAGGACAGTTC	141		
190	ATTCTGGTGTGCTCCGATGACGAGAGACACTGGCAGACCTGGGAGCAACAAGCGGAGTTC	249		
142	CTGCTGGCGGTGTGTGGATTCGCACTGATCTTGTGTAACGTGTGGCATTCCTCCCTCAATC	201		
250	CTCCGCGCGGTGATGGGTTCGCACTGATCTGGGCAATGTGTGGCCCTTCCTCCGTAATC	309		
202	TGTTAACGAAAGGAGGCGGCGGTCTCTGATTCGCCGTACTGCGTATCTCTGTTGGC	261		
310	TGCTATTCGAACGGAGGCGGCGCTCTCTGTGGCTCTACTGCTCTTCTCATCTTTCGGT	369		
262	GGGCTGCGGCTGTTCTTCTCTGGAATGCGGTGGGCGCACAGTACACCGCTGGGCGCTCTC	321		
370	GGAGTGGCCCTGTTCTACATGAGGTGGCGCTGGGCGACGTTCCACCGATGTGTGGCTTC	429		
322	ACTCTCTGAAACGGATGTGCCCGCGCTTAAAGGTGTGGCTATGCATCTGCATGATC	381		
430	AGCATCTGGAAGCGCATGTGTCGGGCTCTAAAGGCTGGGGCTATGACATCTGGCTATTC	489		

QY	382	TACATCTACATGGGCACTACTACAAACACGATTCATCGGATGGGGGCTGTATTACTCATC	441
Db	490	GACATTATATATGGGCATGTACTACAAACGATTTATTCGGCTGGGGGTATATACCTCTTC	549
QY	442	GCTTCTCCGGGTGTATTAACCTGTGTGTCGATAGAACCACTCGCAGCAACAGTAGAAC	501
Db	550	GCCTCGTTCAATCCA-----AGTTGGCGGTGAGACCTGTGGGATTAATCCTCGAAC	600
QY	502	ACGCCGCTGTGCACGCCGCTCACTCACCTCAGACTAATCCTAACTCTTACACCGGG	561
Db	601	ACTGAGAACTCATGTGCAGGTGACCAGTAGAGAACTTCAAGGAACGTGGCCATCCCGGCC	660
QY	562	AAGGAGTCTTCGAAACGTAATGTATTTGAGAGACGACAAGTCTAAGCGCTGGATGATCAT	621
Db	661	AAGGAGTCTTGTGAACGCAAAAGGTTTTGGAGAGCTACAAAGGCAACGGGCTTGACTATG	720
QY	622	GGCGCGATCAAGCCGTCGCTGGCTGTGTGTGTTCGGGGCTTTGTCTCTGTCTACTTTC	681
Db	721	GGTCGGGTGAAGCCACGCTGGCACTCGCTTCGGGGTCTTTGTCTGTGTCTACTTTC	780
QY	682	TCTTTGTGGAAGAGAGTAGAGAGTGTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCG	741
Db	781	TCCCTGTGGAAGGAGGTCCGACAGTCCCGGAAGGGTGTGGGTGACCGCTCGCTCTCT	840
QY	742	TACGTTGTCGTCGATCTTCTGTGGCCGAGAGCGTCACGCTTCCAGAGGACGACGAGGC	801
Db	841	TATGTGGTCTAATCATCTCTGCTGTGTATGAGAGATTTTCCCTGTCGCCGGCGGACGAGGC	900
QY	802	ATACGCTACTACCTTACCACAGAGTGGCACAATTTGCAAAACTCTAAGGTATGATTTGAC	861
Db	901	ATCAAGTACTACTAACCCCGGAGTGGCACAACGTAAGAGTACTCAAAAGTCTGGATTTGAC	960
QY	862	GGCGATCCGAGATTTTCTCTCGTGTGGTCCCGGGTTCCGGAACCTTACTGGGCGTCTCC	921
Db	961	GCCTGATCCAGATTTTCTTCTCCCTTGGCCCCGGATTGGAAACCTGTGCTGGCCCTGTCC	1020
QY	922	AGCTACAAAGTTTCACAAACAACTGTCTACAGGAGGAGCGCTCATCACTTCTTTCATCAAC	981
Db	1021	AGCTACAAAGTTTCACAAACAACTGTCTATCGCGATGCTCTATCAACGACGATCAAC	1080
QY	982	TGCTTGACACAGCTTCTCTGTGTGTTTCTGTATTTTCTGTGGTTTTTGGGTACATGGCGAC	1041
Db	1081	TGCTTGACACAGTTTCTTCTGGCCGCTTGTGTCAATCTTCTCGTTTTTGGGGTATCATGGCTAC	1140
QY	1042	GTTTCAGACAAGAGCATGTAGAGAGGTTGGCCCTCGAAGGCCCTCGACTGTGTATCGTGT	1101
Db	1141	GTTCAAAAGACCTTCATGTACAGAGGTGGGCTTGGAGGGTCCGGGGCTGTGTTCATCGTT	1200
QY	1102	TACCCGAGGCCATGCGCCACCATGACCGGCTCCGTTCTGGGCCATCTTCTCTCTC	1161
Db	1201	TACCCGAGGCCATAGCCACCATGAGTGGCTCGGTCTGTGGAGCATCATCTTCTCTCTG	1260
QY	1162	ATGCTTATTACCTCGGGACTGTACAGTACTTTTGGAGGCTTGTGAGGCAAGTACCAAGGCT	1221
Db	1261	ATGCTGATTACCTCGGGACTGTACAGCACTTTTGGCGGATTGGAGGCGCATATTAACACCG	1320
QY	1222	CTTTCGAGCAATATCTCTGAGTGTTAGCAGACATCCGGAAGTATTTGTGGCTGTACTGT	1281
Db	1321	CTGTGCGAGAGTATTCGCGAGTGTATTTGGACAGGCGGCAAGGAGCTGTGTCTCTCTCTC	1380
QY	1282	CTTCTGTTTCATCTAATTTTGGGCTGTGCCACACACCATATACGTTGTGTATACCTGTA	1341
Db	1381	CTGGCTTTTCATCTTCTGTGGGCCCTTCCCAAGATGACCTACGGGTGGGTGTGTGTCTC	1440
QY	1342	GACCTACTCAATGTGTATGGCCCTGGATTTGGGATTTAATTCGTGTATTTGTGCGAGCT	1401
Db	1441	AACCTTCGTAATGTGTACGAGACCGGGTTGGCATCCTCTTTTGTGTGTCTTGTGTGAGCA	1500
QY	1402	GCCGCGTGTGCTGGGTGTATGTGCGTCGACCGGTTCTGTGAAGATGTGAGACCATGTGTG	1461
Db	1501	GCCGAGTCTTTTGGTTCTACGGAATGAGCCGCTTCACTCGGATGTGGAACAGATGTGTG	1560

QY 1462 GGGACACCCCTGATGATGTTCTGAGAGACCTGTGCTTATACATAGTCCCGTATCTTG 1521
 DB 1561 GCGAGAACCCAGGCTTATCTGCGGACTCTGTGACGTACATACGCGCTGTCTCCG 1620
 QY 1522 CTGGTGTCTGCTGTTCTCCGTTCTGGACACGAGAGATGCTGGCGGGAATACAC 1581
 DB 1621 CTGACCATATGATTTCTCCATCATGAGGCTACAGAGAGATGCTGGCGGAGATCTAC 1680
 QY 1582 TATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1641
 DB 1681 TACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 QY 1642 CCTCTTACATATATACAACTGCTCATAC 1673
 DB 1741 CCATGATACATATATCTACAAAGTTCTTCTGCG 1772

RESULT 5
 US-60-191-681-6790 Application US/60191681
 GENERAL INFORMATION:
 APPLICANT: Li, Peter, M.D.
 TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
 FILE REFERENCE: C1000390
 CURRENT APPLICATION NUMBER: US/60/191,681
 CURRENT FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 30973
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 6790
 LENGTH: 2471
 TYPE: DNA
 ORGANISM: DROSOPHILA
 US-60-191-681-6790

Query Match 50.5%; Score 891.2; DB 63; Length 2471;
 Best Local Similarity 71.7%; Pred. No. 2,1e-212;
 Matches 1185; Conservative 0; Mismatches 458; Indels 9; Gaps 1;

QY 22 CCGCGGCGCCAGCGCGGACCTCTGATCTTCTGCTACACCGGCTCAGAAACCGCTTGG 81
 DB 130 CACACGAGCGCCCGCCAGGCTACCGATCCAGCTGGCGCCCAAGCTGGCCAAACGAGCGC 189
 QY 82 GTGTGTGTGTCTGCTTACCGCGCGGCGGAGAGACTGGGCGAAGGAGAGAGATTC 141
 DB 190 ATTCTGTGTGTCTGCTTACCGCGGCGGAGAGACTGGGCGAAGGAGAGAGATTC 249
 QY 142 CTGT 201
 DB 250 CTCTGT 309
 QY 202 TGTTCACGAATGAGAGCGGCTGCTTCTGATCCGCTACTGCTGTATGCTGTGTGTG 261
 DB 310 TGTTCACGAATGAGAGCGGCTGCTTCTGATCCGCTACTGCTGTATGCTGTGTGTG 369
 QY 262 GGGCGCGGCTGT 321
 DB 370 GGAAGCGCGGCTGT 429
 QY 322 ACTGTGTGAAGAGATGCTGCGCGGCTTAAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 381
 DB 430 ACATGTGTGAAGAGATGCTGCGCGGCTTAAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 489
 QY 382 GACATCTACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 441
 DB 490 GACATCTACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 549
 QY 442 GCTTCTGT 501
 DB 550 GCTTCTGT 600
 QY 502 ACGCGCGT 561

DB 601 ACTGAGAACTGATGAGGTGACAGTGAAGACTTACAGAACTGAGGCGGCGGCG 660
 QY 562 AAGGATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 621
 DB 661 AAGGATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 QY 622 GGGCGGATGAGGCGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 681
 DB 721 GGTGCGGATGAGGCGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 QY 682 TCCCTGTGAGAGAGATGAGGCGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 741
 DB 781 TCCCTGTGAGAGAGATGAGGCGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 742 TACGT 801
 DB 841 TATGT 900
 QY 802 ATACGCTACTACCTTACCCGAGAGTGGCACAATGCAAACTTAAGGTATGATGATGAC 861
 DB 901 ATCAAGTACTACCTTACCCGAGAGTGGCACAATGCAAACTTAAGGTATGATGATGAC 960
 QY 862 GGGGATCCGAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
 DB 961 GCGGATCCGAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 QY 922 AGCTACACAACTTACACAACTTACACAACTTACACAACTTACACAACTTACACAACT 981
 DB 1021 AGCTACACAACTTACACAACTTACACAACTTACACAACTTACACAACTTACACAACT 1080
 QY 982 TGT 1041
 DB 1081 TGT 1140
 QY 1042 GTTTCAGAACAGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1101
 DB 1141 GTTTCAGAACAGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1200
 QY 1102 TACCCGAGGCGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1161
 DB 1201 TACCCGAGGCGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1260
 QY 1162 ATGCTTATATACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1221
 DB 1261 ATGCTTATATACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1320
 QY 1222 CTTTGT 1281
 DB 1321 CTTTGT 1380
 QY 1282 CTTTGT 1341
 DB 1381 CTTTGT 1440
 QY 1342 GACCTACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1401
 DB 1441 GACCTACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
 QY 1402 GCGGCGT 1461
 DB 1501 GCGGCGT 1560
 QY 1462 GGGGACACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1521
 DB 1561 GGGGACACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 QY 1522 CTGGT 1581
 DB 1621 CTGGT 1680
 QY 1582 TATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1641

Db 1681 TACCCGAGTGGAGCTACAGAGTGGGCGGTGCACCTGCTCGGTGCTGCATC 1740
QY 1642 CCTCTTACATATCTACAACTGCTCATAC 1673
Db 1741 CCATGTACATATCTACAAAGTTCTTCTCGC 1772

RESULT 6
US-60-167-217-8786
; Sequence 8786, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1000152
; CURRENT APPLICATION NUMBER: US/60/167, 217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FASTSEQ for Windows Version 4.0
; NO. ID NO: 8786
; LENGTH: 2473
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-217-8786

Query Match 50.5%; Score 891.2; DB 60; Length 2473;
Best Local Similarity 71.7%; Pred. No. 2,1e-212;
Matches 1185; Conservative 0; Mismatches 458; Indels 9; Gaps 1;

QY 22 CCCGCGCCACCGCCGACCTCTGATCTCTCTGCTACACCGGCTCAGAAAACCGTTG 81
Db 133 CACAGAGGCGCCGCAAGGTACCGATCCACTGCGCCCAAGCTGGCCAAACAGAGCGC 192
QY 82 GTGTGTGTGTGCTTACCGCGCGCGCAGCGAGACCTGGCGAAGAGCGAAGTTTC 141
Db 193 ATTCTGTGTGTCTCCGTGACGAGAGAGACTCGCGAGACCTGGGAGAGCGAGTTTC 252
QY 142 CTGCTGGGCGGTGGGATGCGATGGAATCTGTGTAACGTGTGGGATGCCCTACATC 201
Db 233 CTCCTGCGCGATGATGAGTTGCGTCAAGTGGATGCGCAATGTGGGCTTCCGCTACATC 312
QY 202 TGTTCACGAATGAGAGCGGTGCTGCTGATCCCGTACTGCGTTATGCTGTTTGGC 261
Db 313 TGTTCACGAATGAGAGCGGTGCTGCTGATCCCGTACTGCGTTATGCTGTTTGGC 372
QY 262 GGGCTGCGCGTCTTCTTCTGGAATGCGCGTGGGCGAGTACACCGCTGCGGCTGCTC 321
Db 373 GACATGCGCGTCTTCTTCTGGAATGCGCGTGGGCGAGTACACCGCTGCGGCTGCTC 432
QY 322 ACTCTGTGAAAGGATGCGCGCGGTAAAGGTGCGGTATGCGCATGCGATGATC 381
Db 433 AGCATGTGAAAGGATGCGCGCGGTAAAGGTGCGGTATGCGCATGCGATGATC 492
QY 382 GACATCTACATGCGCATGCTACTACAAACAGATCATGATGATGCGGTATGATGATC 441
Db 493 GACATCTACATGCGCATGCTACTACAAACAGATCATGATGATGCGGTATGATGATC 552
QY 442 GCTTCTCTGCGTCTATTAATCTGCTGCTGCGATGAGACAGTGGCAGAACAGTGGAAC 501
Db 553 GCTTCTCTGCGTCTATTAATCTGCTGCTGCGATGAGACAGTGGCAGAACAGTGGAAC 603
QY 502 ACGCGCGTGTGAGCGCGGTGACCTACCTACCTAATCCATACCTCTTCTACACGGCG 561
Db 604 ACTGGAACCTGATGAGGTGACCTACCTAATCCATACCTCTTCTACACGGCG 663
QY 562 AAGGATCTTCTGAGATGATGATGAGAGCAGACAGTCAAGCGCTGATGATGATC 621
Db 664 AAGGATCTTCTGAGATGATGATGAGAGCAGACAGTCAAGCGCTGATGATGATC 723
QY 622 GGGCGGATCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Db 724 GGTTCGGTGAACCGACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783

QY 682 TCCCTTGTGAAGAGATCAGAGATGCTGCAAGTGTGTGTGCTGACACCTGTGCGCCG 741
Db 784 TCCCTTGTGAAGAGATGCTGCAAGTGTGTGTGCTGACACCTGTGCTGCTGCT 843
QY 742 TACGT 801
Db 844 TATGT 903
QY 802 ATAGCTACTACTTACCCAGAGTGGCACAATTTGCAAACTGTAAGTATGATGATGAC 861
Db 904 ATCAAGTACTACTTACCCAGAGTGGCACAATTTGCAAACTGTAAGTATGATGATGAC 963
QY 862 GGGGATCCCAATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
Db 964 GCGGATCCCAATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
QY 922 AGCTACACAGTGTACAAACAGTGTGAGAGAGCGGCTCATCATCTTCTTCTATCAC 981
Db 1024 AGCTACACAGTGTACAAACAGTGTGAGAGAGCGGCTCATCATCTTCTTCTATCAC 1083
QY 982 TCCCTTGTGAAGAGATGCTGCAAGTGTGTGTGCTGACACCTGTGCGCCG 1041
Db 1084 TCCCTTGTGAAGAGATGCTGCAAGTGTGTGTGCTGACACCTGTGCGCCG 1143
QY 1042 GTTCAGAACAGAGATGAGAGTGTGCGCTGCAAGCGCTGAGCATGCTGCTATCCTG 1101
Db 1144 GTTCAGAACAGAGATGAGAGTGTGCGCTGCAAGCGCTGAGCATGCTGCTATCCTG 1203
QY 1102 TACCCGAGCGCATGCGCATGACCGGCTCGGTTGTGGCGCATCTTCTTCTCTC 1161
Db 1204 TACCCGAGCGCATGCGCATGACCGGCTCGGTTGTGGCGCATCTTCTTCTCTC 1263
QY 1162 ATGCTTATTTACCTGGAGTGTACAGTCTTTGAGAGTCTTGAAGAGTCAACAGGCT 1221
Db 1264 ATGCTTATTTACCTGGAGTGTACAGTCTTTGAGAGTCTTGAAGAGTCAACAGGCT 1323
QY 1222 CTGTCGAGAGATATCCCTGAGTGTGAGGACACATGCGGAGTATTTGTGCTGCTAC 1281
Db 1324 CTGTCGAGAGATATCCCTGAGTGTGAGGACACATGCGGAGTATTTGTGCTGCTAC 1383
QY 1282 CTGTCGAGAGATATCCCTGAGTGTGAGGACACATGCGGAGTATTTGTGCTGCTAC 1341
Db 1384 CTGTCGAGAGATATCCCTGAGTGTGAGGACACATGCGGAGTATTTGTGCTGCTAC 1443
QY 1342 GACCTACTAATGTGATGAGCGCTGAGTGTGAGTGTGATTTGCTGAGGCT 1401
Db 1444 AACTTCTGAAATGCTACAGGACCGGTTGGCATCTTGTGTGCTTCTGAGAGCA 1503
QY 1402 GCGGCGGTGCTGAGGATGAGGCGTGCAGCGGTTCTGGAAGATGTGAGACACATG 1461
Db 1504 GCGGCGGTGCTGAGGATGAGGCGTGCAGCGGTTCTGGAAGATGTGAGACACATG 1563
QY 1462 GGGCACACCCCTGATGATGCTGAGAGACCTTGTGCTTACATGATCCCTATTTCTG 1521
Db 1564 GGGCACACCCCTGATGATGCTGAGAGACCTTGTGCTTACATGATCCCTATTTCTG 1623
QY 1522 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581
Db 1624 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683
QY 1582 TATCCCTGATGCTATACCGTGAAGGCGGTGATGAGCGGACACACCGCTGCGCAT 1641
Db 1684 TATCCCTGATGCTATACCGTGAAGGCGGTGATGAGCGGACACACCGCTGCGCAT 1743
QY 1642 CCTCTTACATATCTACAACTGCTCATAC 1673
Db 1744 CCATGTACATATCTACAAAGTTCTTCTCGC 1775

RESULT 7
US-60-360-207-11577
; Sequence 11577, Application US/60360207

RESULT 9
PCT-US00-20638-11
Sequence 11, Application PC/TUS0020638
GENERAL INFORMATION:
APPLICANT: Genaisance Pharmaceuticals
APPLICANT: Denton, R. Rex
APPLICANT: Nandabalan, Krishnan
APPLICANT: Sanchis, Angela
APPLICANT: Duda, Amy
TITLE OF INVENTION: DRUG TARGET ISOGENES: POLYMORPHISMS IN THE SOLUTE
FILE REFERENCE: MMH-0005 PCT SLC6A4-HSERT
CURRENT FILING DATE: 2000-07-31
PCT/US00/20638
PRIOR FILING DATE: 60/146,290
NUMBER OF SEQ ID NOS: 380
SOFTWARE: Patentl Ver. 2.1
SEQ ID NO 11
LENGTH: 1890
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US00-20638-11

Query Match 31.4%; Score 554; DB 1; Length 1890;
Best Local Similarity 59.6%; Pred. No. 7e-128;
Matches 954; Conservative 0; Mismatches 645; Indels 3; Gaps 1;

107 GGCAGCGGAGACCTGGGGCGAAGAGGAGAGAGCTTCCTGGCGGTGGGATTCGAG 166
1230 GGGAGCGGAGACCTGGGGCGAAGAGGAGAGCTTCCTGGCGGTGGGATTCGAG 289
167 TGGATCTGTGTAACGTGGGCGATTCCTTCATCTGTACAGATGAGGCGGTGGT 226
290 TGGACCTGGCAATCTGGGCGCTTCCTTCATCTGTACAGATGAGGCGGTGGT 349
227 TCTGATCCGTACTGCGTTATGCTGTTTGGGCGGTGGCGGTGTTCTTCGTAAC 286
350 TCTCTCCCTTACACCATGAGGCGATTTTGGGCGGTGGCGGTGTTTACATGAGC 409
287 TGGGCGGCGGAGACCGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGG 346
410 TGGACCTGGGAGAGACCGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGG 469
347 CGCTTAAAGTGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGG 406
470 TTTTCAAGTATTTGGTATTCATCTGTACATCTTCCTTTTACATCTTCCTTCTTCA 529
407 ACAGATCATGAGTGGGCGGTGGTATTCATCTGTGCTGCTTCGCGGTCTTAAACTG 466
530 ACACCATCATGCTGGGCGGTGGTATTCATCTGTGCTTCCTTCACGAGCAGCTGCG 589
467 TGGCGCATGAGCAGGCGGAGCAACGAGTGGAGACCGCGGTGGCGGTGGCGGTGG 526
590 GAGCAGCTGGAGAGCTCTGGAGACAGTGGAGCACTGGCAATTAATCTTCGAGGAG 649
527 CACCTGAGACTAATCTTAATCTTCTACACCGGAGAGAGTCTTTCGAGAGTATGAT 586
650 ACATCAGCTGGAGCTTCATTCACGCTGCTGCTGAGAGATTTTACACGCGCCACGCT 709
587 TGGAGCAGCAGTCTTAACGCGCTGGATGAGTGGGCGGAGCAAGCGGTGGTGGCTC 646
710 TGGAGATCAGCAGGCTTAAGGCGCTGACGAGCTGGGCGGATCAGCTGGAGCTGG 769
647 TGGTGTGTGGGCGCTTCTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
770 TCTCATCATCT 829
707 CTGCAAGTGTGTGGTGGAGCTCTGGCGCGGTGAGTGGTGGTGGTGGTGGTGGTGG 766
830 CTGCAAGTGTGTGGTGGAGCTCTGGCGCGGTGAGTGGTGGTGGTGGTGGTGGTGG 889

767 CGAGAGCGGTACCGTTCACAGAGGAGGAGGAGGATACGCTTACCTTACCCAGAGT 826
890 TGGAGGAGTGGACCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 949
827 GGCACAAATTCAGAACTCTAAGGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 886
950 GGCAGAACTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1009
887 TCGTCCCGGAGTGGAGACCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 946
1010 TTGGTCCGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1069
947 GCTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1006
1070 GCTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
1007 TCGTCAATTTCTCGGTTTGGGAGTACATGCGGAGGAGGAGGAGGAGGAGGAGGAG 1066
1130 TTGTCTCTCTCAGAGTGGTGGGAGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1189
1067 TTGGC---CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1123
1190 TGGCCAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1249
1124 TGACCGGCTCCGTTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1183
1250 TGGCAGGCTCCAGCTTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1309
1184 ACAGTACTTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1243
1310 ACAGAGCTTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1369
1244 TGTAGGAGAGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1303
1370 TCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1429
1304 CTCTGCCAGCAGCAGATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1363
1430 CCTGTGATACCTGAGCTTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1489
1364 CTGATTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1423
1490 CGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1549
1424 GCGTGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1483
1550 GCATCAGTCAATTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1609
1484 GAGGAGCTGTTGATCTTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1543
1610 GAGGAGCTGTTGATCTTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1669
1544 TTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1603
1670 TGTAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1729
1604 TAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1663
1730 TGGTATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1789
1664 TGTCTATCATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1705
1790 TGTATCATCATCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1831

RESULT 10
US-09-440-302A-1068
Sequence 1068, Application US/09440302A
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11

```

: CURRENT APPLICATION NUMBER: US/09/440,302A
:
: CURRENT FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053,375
: PRIOR FILING DATE: 1998-03-31
: NUMBER OF SEQ ID NOS: 1193
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1068
: LENGTH: 2099
: TYPE: DNA
: ORGANISM: Homo Sapiens
US-09-440-302A-1068

```

Query Match	31.38;	Score 552.6;	DB 18;	Length 2099;
Best Local Similarity	59.38;	Pred. NO. 1.6e-127;		
Matches 958; Conservative	0;	Mismatches 654;	Indels 3;	Gaps 1

[illegible]

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Db      1180  GCTACCAAGATGCCCTGGTGCACGCGTGGTGAACCTGCATATACAGACCTTCTTCGGGAT 1239
QY      1007  TCGTCATTTTCTCGGTTTGGGGTACATGCGGCAGTTTCAGAACAGAGCATCGAGAGG 1066
Db      1240  TTGTCATCTTACAGTGTCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGCTGAGG 1299
QY      1067  TTGGC---CTGAAGAGCCCTTGACTGGTGTTCATCTGTGTACCCGAGGCCATGCCACA 1123
Db      1300  TGCCCAAAAGACGAGGTCCAGCCCTCCCTTCATACAGCTAATGACGAAGCGCATACACA 1359
QY      1124  TGACCGGCTCGTGTTCGGCCCAATCCTTCCTCCATGATACCTTAATACCTGGGACTGG 1183
Db      1360  TGCCAGCTCCACTTCTTCTTCCATCATCTTCTTCTGATTTATACACGCTGGGCTTGG 1419
QY      1184  ACACTACTTTTGGAGGCTTTGAGCGAGTCACACAGCGCTCTTGGAGCAATATCTCGAG 1243
Db      1420  ACACAGCTTTGGACAGGCTTGGAGGGGGTGATACAGCGCTGCTGATGATAGTGTCCACAG 1479
QY      1244  TGTTAGCGACAGCATGCCAGACTATTGTGGCTGTACTGTCTTGTATCTATATTGGCG 1303
Db      1480  TCTGGGCGCAACGCGCGGAGCGGTTTCCGTGCGCTGCGCGGTATCATACCGCTTCTTGGAT 1539
QY      1304  CTCGCGCCACACACATAGCGTGGTGTATACCTCGTAGACCTACTCATGTGATGGCC 1363
Db      1540  CCTGTGTCACCTGACTTTTGGAGGGGCTCTACGTGTGAAGCTCTGGAGGATATGCCA 1599
QY      1364  CTGATTTGGCGATTCTTATCTGTGTATTGTCTGAGAGCTGCCGGCGTGTGCTGTATG 1423
Db      1600  CGGGGCCCGCAGTGTCTACCTTCCTCCGCGTGATCGAAGCAGTGTGCTGTGTGTTCTATG 1659
QY      1424  GCGTCGACCGGTTCTCTGAGAGATGTGAGACCATGCTGGGGCACACCCCTGGATGTTCT 1483
Db      1660  GCATCACTCAATCTCTCCAGCGCATGGAAGAAATGCTGCGCTTACGACCCGGGGGTTCT 1719
QY      1484  GGAGGACCTGTGTGCTTACATCAATGATCCCGATTTCTGCTGTGCTGTCTGTTCCG 1543
Db      1720  GGAGGATCTGCTGGGTGGCCATCAAGCCCTCTGTTTCTCTTCTTATCATATTGGACGTTTC 1779
QY      1544  TTCTGGCCACAGAGAGATGCTCGGGGGGATACACTATCTCCCTCATGCTCTATCACCG 1603
Db      1780  TGATGAGCGCCGCCACAACTACGACTTTTCCAAATTAATATATCTTACGGAGTATCATCT 1839
QY      1604  TAGGCTGGGTGATGACCGGCACACCCGCTCTGTCGATTCCTTTTACATTAATCTACAAC 1663
Db      1840  TGGCTTACTGATGAGAACCTCATCTTTCATTTTGCATCCCAACATATATCTTATCGGT 1899
QY      1664  TGTCTATCATCTCTCGGCATTTGCATCAACCGCATCAGACAAATCCACGTCGCGA 1718
Db      1900  TGATCATCTACTCCAGGACATTTTAAAGAGCGTATTATTATTAAGATTATACCCGGA 1954

RESULT 11
US-09-440-302B-1068
; Sequence 1068, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chukashv, Alex
; APPLICANT: Lukashv, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440, 302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053, 375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1068
; LENGTH: 2099
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-440-302B-1068

;31.3%; Score 552.6; DB 18; Length 2099;

```



```
QY 287 TGGCGCTGGCCAGTACACCGCTGCGCTGCTCTCTCTGGAAGGATCTGCCCG 346
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 TCGACCTGGGAGACGTACACCGGAATGGATGATTTCAATATGAGGAANAATCCCGA 469
QY 347 CGCTTAAAGGTGTGGCTATGCCATCTGATGATGACATCTACATGGGCATGTACTACA 406
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 TTTTCAAAGGATGGTATGCCATCTGATCTGATCTGCTTTTACATTTCTTCTCTACA 529
QY 407 ACAGCATATGAGTGGGCTGTATTAOCGTATGCTGCTGCTGCTATTAACCTG 466
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 ACACCATATATGCTGGGCTGTATTAOCGTATGCTGCTGCTGCTATTAACCTG 589
QY 467 TGTGTCATGAGACAGCTGCGACAGAGTGAACACCGCTGTGCAAGCGGCTACCT 526
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 GGACCAAGCTGCAAGAACTCTGAGACAGTGGCACTGCAACCAATTAATTTCTCGAGACA 649
QY 527 CACCTCAACATTAATCTTAATCTTACACGCGGCAAGAGTCTTTCAGACGTAAATGAT 586
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 650 ACATCACTGGACCTTCATTCACGTCCTGCTGAAAGAAATTTTACACGCGCCACGTC 709
QY 587 TGGACGACGACAAAGTCTAAGGCTGAGATGACATGGGCGCATCAAGCGCTGCGCTC 646
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 710 TGCAGATCAACCGGCTCTAAGGGGCTCAAGACCTGGGGGCTACAGCTGGCGCTGGCC 769
QY 647 TGTGTGTGTGGGGCTTTTGTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 770 TCTGATCATGCTGTATCTTCACTGTTATCTACTTACATCTGGAAGCGCTCAAGACCT 829
QY 707 CTGGCAAGTGTGTGGGTGACAGCTTGCGCCCTAGCTGCTGCTGCTGCTGCTGCTG 766
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 830 CTGGCAAGTGTGTGGGTGACAGCTTGCGCCCTAGCTGCTGCTGCTGCTGCTGCTG 889
QY 767 CGAGAGGCTGACGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 826
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 890 TGAAGGGGTGCCACCTCCCTGAGAGCTGAGAGGGGTGTCTCTCTACTTGAACCAACT 949
QY 827 GGCACAAATGTCAAACTCTAAGGATAGGATGACGCGGAGATCCAGATTTTCTCTGCG 886
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 950 GGCAGAAATCTCTGTGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1009
QY 887 TCGGTCGCGGGTGGGAACCTACGCGGCTCTCCAGCTACACAAGATTTCAACCAACT 946
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1010 TTGGTCGCGGGTGGGAACCTACGCGGCTCTCCAGCTACACAAGATTTCAACCAACT 1069
QY 947 GCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1006
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1070 GCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
QY 1007 TCGTCATTTTCTCGGTTTGGGATACATGCGCGACGTTCCAGACAAGAGCATGAGAGG 1066
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1130 TTGTATCTTCAACATGCTGCGGTACATGGCTGAGATGAGCAATGAAGTGTCTGAGG 1189
QY 1067 TTGGC---CTGGAAGCCCTGAGACGTGCTGTATGCTGTACCCCAAGGCGCATGCGCACA 1123
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1190 TGGCCAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1249
QY 1124 TGACCGGCTGCTGTGGGCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1183
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1250 TGGCAGGCTGCACTTTCTTGGCAGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1309
QY 1184 ACAGTATTTTGGAGGCTTGAAGGAGTACACAGGCTCTTGGCAGCAATATCTCGAG 1243
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1310 ACAGCAGCTTGGAGGCTTGGAGGAGTACACAGGCTCTTGGCAGCAATATCTCGAG 1369
QY 1244 TGTGAGGAGATGCGCAAGTATTTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1303
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1370 TGTGAGGAGATGCGCAAGTATTTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1429
QY 1304 CTCTCCACGACGACATACGCTGTGTATATACCTGTGAGACCTTACATGTATGAGG 1363
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1430 CCTGTGATACCTGCTTTTGGAGGGGCTTACGTGTGTGAGGCTGTGTGAGGAGTATGCA 1489
QY 1364 CTGATTTGGCATTTCTATCTGTGTATTTGTGAGGCTGCGCGCTGTGTGTGTATG 1423
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Db 1490 CGGGGCGGAGAGTGTCTACTGTGCGGTGATGAGAGCAGTGTGTGTGTATG 1549
QY 1424 GCGTGACCGGCTTCTCTAAGATGTGAGGACATCTTGGGACACCCCTGGATGCT 1483
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1550 GCATACGTAGTGTGACGAGGAGTGAAGAAATGCTGGCTTCCCGGGGGGTGCT 1609
QY 1484 GGAGGACCTGTGTGCTTACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1610 GGAGGATGTGCTGGGTGGGACATGACCCCTCTCTCTCTCTCTCTCTCTCTCTCT 1669
QY 1544 TTTGCGACACGAGAGATGCTGTGGGCGGGAATACCATTCCTCATGCTTACCG 1603
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1670 TGTATGAGCGCGGACACATACGACTTTTCAATATTAATTAATCTTACGAGTATCATCT 1729
QY 1604 TAGGCTGGGTATGACCGGCGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1730 TGGGTACTGATGAGAACTTCTATCTTTCATTTGATGCTCCACATATTAATGCTTATGCTG 1789
QY 1664 TGTCTATCATCTCTGCAATTTGATCAACCGCATCAAGACA 1705
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1790 TGTATCATCTCTCCAGGACATTTAAAGCGATTAATTAATAA 1831
```

```
RESULT 14
US-60-226-176-2040
; Sequence 2040, Application US/60226176
; GENERAL INFORMATION:
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Malsen, Gareth
; APPLICANT: Townley, David
; APPLICANT: Morris, MacDonald
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
; FILE REFERENCE: GX-0013-1 P
; CURRENT APPLICATION NUMBER: US/60/226,176
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2447
; SOFTWARE: PERL Program
; SEQ ID NO 2040
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GB:NM_001045.1
US-60-226-176-2040
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Query Match 31.3%; Score 552.4; DB 66; Length 1893;
Best Local Similarity 59.5%; Pred. No. 1.8e-127;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

```
QY 107 GGCAGCGGAGACCTGGGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 166
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 230 GGGAAAGGAGACCTGGGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 289
QY 167 TGGATCTTGTAACTGTGCGGATTCCTCTATCTGTTTACAGAAAGAGGAGGAGGAG 226
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 290 TGGAGCTGGGCAATGTGCGGCTTCCCTCATATGTTTACAGAAAGAGGAGGAGGAG 349
QY 227 TCTGATCCCGTACTGCTTATGCTGTGTTTGGCGGAGCTGCGCTGTTCTTCTGAGAC 286
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 350 TCTCTCTCCCGACACCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 409
QY 287 TGGCGCTGGGCGAGTACACCGGCTGCGGCTGCTCTCTGGAAGAGGATGCGCCCG 346
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 TCGCACTGGAGATGACACCGAAATGATGATTTCAATATGAAGGAAATCTGCCGA 469
QY 347 CGCTTAAAGGTGTGGCTATGCCATCTGATGATGACATCTACATGGGCATGTACTACA 406
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 TTTTCAAAGGATGGTATGCCATCTGATCTGATCTGCTTTTACATTTCTTCTCTACA 529
QY 407 ACAGCATATGAGTGGGCTGTATTAOCGTATGCTGCTGCTGCTATTAACCTG 466
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 530 ACACCATCATGCGCTGGGGCTATACCTATCTCTCTTCAAGGACGACGCTCCCT 589
OY 467 TGCCTGCATGAGACGCTGCGACGACGATGGAACAGCGCGCTGACGCGGTCACCT 526
Db 590 GGACCAAGCTGCAAGACTCTGGAACACTGGCAACGACCAATTAATCTCTCGAGGACA 649
OY 527 CACCTCAGACTATCTTAATCTCTTACACCGCGGAGAGATTCTTCAAGCAATATGAT 586
Db 650 ACATCAGCTGGAGCCCTCCATTCACAGCTCCCTGCTGTAAGAAATTTTACAGCGCCAGCTGC 709
OY 587 TGGAGCAGCACAAGTCTAAAGCGCTGAGATGACATGGGGCCGATCAAGCCGCTGCTGC 646
Db 710 TGCATATCCACCGGCTTAAGGGGGCTCCAGGACCTGGGGGGCATCACTGGACGCTGCC 769
OY 647 TGTGTGTGTGGGGGCTTGTCTGCTGCTATCTCTCTTGGGAAGAGTCAGGAGTG 706
Db 770 TCTGCATCATGCTGATCTTCTACTGTATCTTACCTTACAGCTTGGGAAGGCGTCAACCT 829
OY 707 CTGGCAAGGTGGTGGGTGAGACGCTCTGCCCCCTGACCTGGGTGCTGATCTCTGCTG 766
Db 830 CTGGCAAGGTGGTGGGTGAGACGACCTTCCCTTATATCATCTTCTGCTGCTGCTG 889
OY 767 CGAAGAGCGCTACGCTTCCAGAGGAGCGAGGCGATACGTAACCTTACCCAGAGT 826
Db 890 TGAAGGGGTGCCACCTCTGAGGCTGAGGGGGTCTCTCTTCTACTTGAACCAAT 949
OY 827 GGCACAAATGGCAAACTAAGGTATGATGACCGGCGATCCGAGATTTCTTCTGCG 886
Db 950 GGCAGAACTCTGGAGAGAGGGGTGATGATGACCGCTCGATCTTCTTCTCTC 1009
OY 887 TGGTCCCGGGTTCGGAACCTACTGCGCTCTCCAGCTACAACAGTCAACACACAT 946
Db 1010 TTGGTCCGGGCTTTGGGGTCTGCTGCTGCTTTGCTAGCTACACAAGTTCACAAACAT 1069
OY 947 GCTAAGAGGAGCGGCTCATCACTCTTCTTATCACTGTTGACACGCTTCTGCTGCT 1006
Db 1070 GCTACCAAGATGCTCCGTGGTACGAGCGTGTGATGATGAGAAATGATGTCTGAGG 1129
OY 1007 TCGTATTTTCTGGGTTTGGGGTACATGGCGCAGCTTACAGAACAGAGCTGAGAGG 1066
Db 1130 TTGTCACTTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1189
OY 1067 TTGGC---CTCGAAGCCCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
Db 1190 TGGCCAAAGACGAGAGTCCAGCTCTCTTCAATCAGATGAGAAAGGATGCGCAACA 1249
OY 1124 TCAACGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
Db 1250 TGCACGCGTCCACTTCTTGGCATCATCTTCTTGTGATGATGATGATGATGATGATG 1309
OY 1184 ACAGTACTTTTGGAGTCTTGGAGGCGATGACACAGGCTCTTGGAGCAATATCTCGAG 1243
Db 1310 ACAGCAGCTTTCAGGCTTGGAGGGGATGATCAGGCTGCTGCTGCTGCTGCTGCTGCTG 1369
OY 1244 TGTTAAGCAGCATGCGAAGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
Db 1370 TCTGGGCCAAGGCGCGGAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429
OY 1304 CTCTGCCACCAACACATAGGTGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1363
Db 1430 CCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1489
OY 1364 CTGATGAGGATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
Db 1490 CGGGGCGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
OY 1424 GCGTGCACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483
Db 1550 GATACCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1609
OY 1484 GAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1543
Db 1610 GGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1669

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OY 1544 TTCTGGCACACGAGGATGCTGCGGGGAATACACCTATCCATGCTGATTCACCG 1603
Db 1670 TGAATGACCCCGCACACTACTACGACTTTTCCAAATATATATCTTACTGAGATATCT 1729
OY 1604 TAGGCTGGGTGATGACCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663
Db 1730 TGGGTACTAGATGAGAACCTCATCTTTCATTGCTATCCCAATATATAGCTTATCGCT 1789
OY 1664 TGTCTATCACTCTGCGCAATTGCTATCACCAGCATCAAGACA 1705
Db 1790 TGATCATCACTCCAGGACATTTAAAGACGCTATTTATTTAAA 1831

RESULT 15
US-60-226-176-2045
: Sequence 2045, Application us/60226176
: GENERAL INFORMATION:
: APPLICANT: Ring, Huijun Z.
: APPLICANT: Malsen, Gareth
: APPLICANT: Townley, David
: APPLICANT: Morris, MacDonald
: TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated with ADME Genes
: FILE REFERENCE: GX-0013-1 P
: CURRENT APPLICATION NUMBER: US/60/226,176
: CURRENT FILING DATE: 2000-08-16
: NUMBER OF SEQ ID NOS: 2447
: SOFTWARE: PERL Program
: SEQ ID NO 2045
: LENGTH: 1893
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: SLC6A4_cds.1
US-60-226-176-2045

Query Match 31.3% Score 552.4: DB 66: Length 1893:
Best Local Similarity 59.5% Pred. No. 1,8e-127:
Matches 933: Conservative: 0: Mismatches 646: Indels 3: Gaps 1:

OY 107 GCGAGCGGAGACCTGGGCGGAGAGGACGAGTCTGCTGCGGCTGCTGCTGCTGCTGCTG 166
Db 230 GGAACGCGGAGACCTGGGCGGAGAGAGGATGATTTCTTCTGCTGCTGCTGCTGCTGCTG 289
OY 167 TGGATCTTGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 226
Db 290 TGGACCTGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
OY 227 TCTGTATCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 286
Db 350 TCTCTCTCCCTTACACCATCATATGCGCATTTTGGGGGAATCCGCTTTTACATGAGAC 409
OY 287 TGGCGCTGGGCGAGTACCAACCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 346
Db 410 TCCGACTGGGAGGATGACACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 469
OY 347 CGCTTAAAGGTGTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 406
Db 470 TTTTCAAGAGGATTTGTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTA 529
OY 407 ACACGATCATGCGATGGGGGCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 466
Db 530 ACACGATCATGCGATGGGGGCTATATCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
OY 467 TGTGCTCATGAGACCTGCTGCAACGAGTGAACAGCGCGCTGCTGCTGCTGCTGCTGCTG 526
Db 590 GGAACGCTGCAAGAACTCTGGAACACGTGCAACTGCAACAAATTAATCTCTCGAGGACA 649
OY 527 CACCTCAGACTAATCTTCTTACACCGGCGAAGAGTCTTTCGAACGTAATGTAT 586
Db 650 ACATCAGCTGAGACCTTCATTCACGCTCCCTGCTGAAGAAATTTTACAGCGCGACGCTGC 709

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QY 587 TGGAGCAGACAGTCTTAACGGCCCTGGATGACATGGGGGCCATCAAGCCGCTGGCTC 646
DB 710 TGCAGATCCACCGGCTTAAGGGGCTCCAGGACCTGAGGGGCGATCAGCTGGACGGCCC 769
QY 647 TGTGTCTGTCCGGGCTTGTCTCTGCTACTTCTCTTGGAAAGAGTCCAGAGT 706
DB 770 TCTGCTCATGCTGATCTTCACTGTATCTACTGATCTGGAAGGCGTCACACCT 829
QY 707 CTGGCAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 766
DB 830 CTGGCAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 889
QY 767 CGAAGAGCGCTCAGCGCTTCCAGAGCGAGGAGGCGATACCTACTTACCCAGAGT 826
DB 890 TGAGGGGTGCCACCTCCCTGGAGGCTGGAGGGGTCTCTCTTCTACTTGAAGCCCAATT 949
QY 827 GGCACAAATTGCAAAACTTAAGGTATGATTTGACGGCGCATCCAGATTTCTTCTCCG 886
DB 950 GGCAGAACTCTGGAGAGAGGGGTGTGATGATGACCGCGCTCAGATCTTCTCTCTC 1009
QY 887 TCGGTCCCGGTTTGGAACTTACTGCGCTCTCCAGTACAAGAGTTCAACAACT 946
DB 1010 TTGGTCCGGGCTTTGGGGTCTGCTGCTGCTTGTGCTAGCTACACAGTTCAACAACT 1069
QY 947 GCTACAGGAGCGGCTCATCTTCTTATCAACTCTTGGACACGCTTCTGCTGTT 1006
DB 1070 GCTACCAAGATGCTCCCTGTGACAGGCTGTGATGATGATGAGAGCTTCTGCTGGAT 1129
QY 1007 TGTCTATTCTTCTGCTTTTGGGGTACATGGCGCAGCTTCAAGAACAGACATCGAGAG 1066
DB 1130 TTGTCTATCTTCAAGAGTCTGGTGTACATGGCTGAGATGAGAAATGTGTCTGAGG 1189
QY 1067 TTGGC---CTGAAGGCGCTGAGTGTGTTATGCTGTATCCCGAGGCGCATCGCCACA 1123
DB 1190 TGGCCAAAGACGACAGTCCACGCTCTTCTATCAGCTATGACAGAGCATAGCCACA 1249
QY 1124 TGAACGGCTCGTGTGTTGGGCTATCATCTTCTTCTATGCTTATACCTGGGACTTG 1183
DB 1250 TCCAGCGCTCACTTCTTCTGCTATCATCTTCTTCTGATGTTAATCAGCTGGGCTTG 1309
QY 1184 ACAGTACTTTGAGAGTCTTGAAGGAGTACACAGGCTTGTGCGAGAAATATCTCGAG 1243
DB 1310 ACAGCAGCTTTCAGAGCTTGAAGGGGTATCAGGCTGTGCTGATGAGTTCCACACG 1369
QY 1244 TGTAGGAGAGATGCGAAGTATTTGGCTGTACTGCTTCTGTTCACTATATTTGGC 1303
DB 1370 TCTGGGCCAAGGCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1429
QY 1304 CTCTGCCACACACACATACGCTGTATACCTGCTAGACCTACTCAATGTGTATGCC 1363
DB 1430 CCTGTGTCACCTGACTTTTGGAGGGGCTTACGTGTGTAAGCTGTGAGAGTATGCCA 1489
QY 1364 CTGSAATTGGGANTTCATTCGTGTATTTGCTGAGGCTGCGGCTGCTGGGTATG 1423
DB 1490 CGGGGCGCGCAGTCTGCTACCTGTGCGCTATGCAAGCAGTGTGCTGTGTATG 1549
QY 1424 GCGTGCACCGGTTCTCTGAAGATGTAGAGACCATGCTGGGCGACACCCCTGATGGTCT 1483
DB 1550 GCATCACTCAAGTTCTGACAGGAGCGTAAGAAATGCTGCGCTTCAAGCCGGGGTGTCT 1609
QY 1484 GGAGGACCTGTGTCTTACATCAAGTCCGTAATCTTCTGCTGTGCTGTGTCTCGG 1543
DB 1610 GGAGGATCTGTGGTGGCCATCAGCCCTGTCTTCTCTGTTCAATTTGCAGTTTC 1669
QY 1544 TTCTGGCAGACGAGATGCTCGGGGGGATATACACTATCCCTCATGTCTATCAGCG 1603
DB 1670 TGTATAGCCCGCCACACATACACTTTTCAATATATATATCTTACTGAGATATCATCT 1729
QY 1604 TAGGCTGGGTATGACCGGACACGCTGCTGCTGCTTCTTACATATATCAAAAC 1663
DB 1730 TGGGTTACTGATAGAACCTTATCTTTCATTTGCTATCCCGACATATATAGCTTATCGGT 1789
QY 1664 TGCTCATCATCTCTGGCAATTGATCAACCGCATCAAGCAA 1705

DB 1790 TGTATCATCTCAGGAGCATTTTAAAGACGTATTTAA 1831

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